

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/576,439  
Source: IFWP  
Date Processed by STIC: 5/1/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/576,439

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
  
- 11        Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown."        Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/576,439

DATE: 05/01/2006

TIME: 09:45:10

Input Set : A:\Seq.ST25.txt

Output Set: N:\CRF4\05012006\J576439.raw

3 <110> APPLICANT: Theratechnologies Inc.  
 4 Lussier, Bruno  
 5 Vachon, Luc  
 6 Allas, Soraya  
 7 Abribat, Thierry  
 9 <120> TITLE OF INVENTION: Selection and treatment of patients suffering from wasting  
 11 <130> FILE REFERENCE: 09555.0151USWO  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/576,439  
 14 <141> CURRENT FILING DATE: 2006-04-20  
 17 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/001843  
 18 <151> PRIOR FILING DATE: 2004-10-20  
 20 <150> PRIOR APPLICATION NUMBER: 60/512,198  
 21 <151> PRIOR FILING DATE: 2003-10-20  
 23 <160> NUMBER OF SEQ ID NOS: 7  
 25 <170> SOFTWARE: PatentIn version 3.3  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 30  
 29 <212> TYPE: PRT  
 30 <213> ORGANISM: Artificial sequence  
 32 <220> FEATURE:  
 33 <223> OTHER INFORMATION: GRF peptide  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: VARIANT  
 38 <222> LOCATION: (1)..(1)  
 39 <223> OTHER INFORMATION: Xaa = Tyr or His  
 41 <220> FEATURE:  
 42 <221> NAME/KEY: VARIANT  
 43 <222> LOCATION: (2)..(2)  
 44 <223> OTHER INFORMATION: Xaa = Val or Ala  
 46 <220> FEATURE:  
 47 <221> NAME/KEY: VARIANT  
 48 <222> LOCATION: (8)..(8)  
 49 <223> OTHER INFORMATION: Xaa = Asn or Ser  
 51 <220> FEATURE:  
 52 <221> NAME/KEY: VARIANT  
 53 <222> LOCATION: (13)..(13)  
 54 <223> OTHER INFORMATION: Xaa = Val or Ile  
 56 <220> FEATURE:  
 57 <221> NAME/KEY: VARIANT  
 58 <222> LOCATION: (15)..(15)  
 59 <223> OTHER INFORMATION: Xaa = Ala or Gly  
 61 <220> FEATURE:  
 62 <221> NAME/KEY: VARIANT

Does Not Comply  
 Corrected Diskette Needed

give source of GRF  
 (see item 11 on Error  
 summary  
 sheet)

## RAW SEQUENCE LISTING

DATE: 05/01/2006

PATENT APPLICATION: US/10/576,439

TIME: 09:45:10

Input Set : A:\Seq.ST25.txt

Output Set: N:\CRF4\05012006\J576439.raw

63 <222> LOCATION: (18)..(18) ✓  
 64 <223> OTHER INFORMATION: Xaa = Ser or Tyr  
 66 <220> FEATURE:  
 67 <221> NAME/KEY: VARIANT  
 68 <222> LOCATION: (24)..(24) ✓  
 69 <223> OTHER INFORMATION: Xaa = Gln or His  
 71 <220> FEATURE:  
 72 <221> NAME/KEY: VARIANT  
 73 <222> LOCATION: (25)..(25) ✓  
 74 <223> OTHER INFORMATION: Xaa = Asp or Glu  
 76 <220> FEATURE:  
 77 <221> NAME/KEY: VARIANT  
 78 <222> LOCATION: (27)..(27) ✓  
 79 <223> OTHER INFORMATION: Xaa = Met or Ile or Nle  
 81 <220> FEATURE:  
 82 <221> NAME/KEY: VARIANT  
 83 <222> LOCATION: (28)..(28) ✓  
 84 <223> OTHER INFORMATION: Xaa = Ser or Asn  
 86 <220> FEATURE:  
 87 <221> NAME/KEY: VARIANT  
 88 <222> LOCATION: (30)..(30)  
 89 <223> OTHER INFORMATION: Xaa = amino acid sequence of 1 up to 15 residues or is a bond  
 91 <400> SEQUENCE: 1  
 W--> 93 Xaa Xaa Asp Ala Ile Phe Tyr Xaa Ser Tyr Arg Lys Xaa Leu Xaa Gln  
 94 1 5 10 15  
 W--> 97 Leu Xaa Ala Arg Lys Leu Leu Xaa Xaa Ile Xaa Xaa Arg Xaa  
 98 20 25 30  
 101 <210> SEQ ID NO: 2  
 102 <211> LENGTH: 44  
 103 <212> TYPE: PRT  
 104 <213> ORGANISM: Homo sapiens  
 107 <220> FEATURE:  
 108 <221> NAME/KEY: MISC\_FEATURE  
 109 <222> LOCATION: (44)..(44)  
 110 <223> OTHER INFORMATION: Leu residue is capped with an unsubstituted amide moiety  
 112 <400> SEQUENCE: 2  
 114 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln  
 115 1 5 10 15  
 118 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly  
 119 20 25 30  
 122 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu  
 123 35 40  
 126 <210> SEQ ID NO: 3  
 127 <211> LENGTH: 44  
 128 <212> TYPE: PRT  
 129 <213> ORGANISM: Artificial sequence  
 131 <220> FEATURE:  
 132 <223> OTHER INFORMATION: Amino acid sequence of human GRF  
 134 <400> SEQUENCE: 3

*variable length, not permitted - see item 5*  
*on*  
*even summary sheet*  
*Xaa can only represent a single amino acid, nothing else*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/576,439

DATE: 05/01/2006

TIME: 09:45:10

Input Set : A:\Seq.ST25.txt

Output Set: N:\CRF4\05012006\J576439.raw

136 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln  
 137 1 5 10 15  
 140 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly  
 141 20 25 30  
 144 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu  
 145 35 40

148 &lt;210&gt; SEQ ID NO: 4

149 &lt;211&gt; LENGTH: 29

150 &lt;212&gt; TYPE: PRT

151 &lt;213&gt; ORGANISM: Homo sapiens

154 &lt;220&gt; FEATURE:

155 &lt;221&gt; NAME/KEY: MISC\_FEATURE

156 &lt;222&gt; LOCATION: (29)..(29)

157 &lt;223&gt; OTHER INFORMATION: Arg residue is capped with an unsubstituted amide moiety

159 &lt;400&gt; SEQUENCE: 4

161 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln  
 162 1 5 10 15

165 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg

166 20 25

169 &lt;210&gt; SEQ ID NO: 5

170 &lt;211&gt; LENGTH: 29

171 &lt;212&gt; TYPE: PRT

172 &lt;213&gt; ORGANISM: Artificial sequence

174 &lt;220&gt; FEATURE:

175 &lt;223&gt; OTHER INFORMATION: Amino acid sequence of minimum active core of human GRF

177 &lt;400&gt; SEQUENCE: 5

179 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln  
 180 1 5 10 15

183 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg

184 20 25

187 &lt;210&gt; SEQ ID NO: 6

188 &lt;211&gt; LENGTH: 15

189 &lt;212&gt; TYPE: PRT

190 &lt;213&gt; ORGANISM: Artificial sequence

192 &lt;220&gt; FEATURE:

193 <223> OTHER INFORMATION: Amino acid sequence corresponding to positions 30 to 44 of  
 human

194 GRF

196 &lt;400&gt; SEQUENCE: 6

198 Gln Gln Gly Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu

199 1 5 10 15

202 &lt;210&gt; SEQ ID NO: 7

203 &lt;211&gt; LENGTH: 44

204 &lt;212&gt; TYPE: PRT

205 &lt;213&gt; ORGANISM: Artificial sequence

207 &lt;220&gt; FEATURE:

208 &lt;223&gt; OTHER INFORMATION: Modified GRF peptide

211 &lt;220&gt; FEATURE:

212 &lt;221&gt; NAME/KEY: MISC\_FEATURE

213 &lt;222&gt; LOCATION: (1)..(1)

## RAW SEQUENCE LISTING

DATE: 05/01/2006

PATENT APPLICATION: US/10/576,439

TIME: 09:45:10

Input Set : A:\Seq.ST25.txt

Output Set: N:\CRF4\05012006\J576439.raw

214 <223> OTHER INFORMATION: Tyr residue is linked to an hexenoyl-trans-3 moiety  
216 <220> FEATURE:  
217 <221> NAME/KEY: MISC\_FEATURE  
218 <222> LOCATION: (44)..(44)  
219 <223> OTHER INFORMATION: Leu residue is capped with an unsubstituted amide moiety  
221 <400> SEQUENCE: 7  
223 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln  
224 1                   5                   10                   15  
227 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly  
228                   20                   25                   30  
231 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu  
232                   35                   40

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/576,439

DATE: 05/01/2006  
TIME: 09:45:11

Input Set : A:\Seq.ST25.txt  
Output Set: N:\CRF4\05012006\J576439.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1, 2, 8, 13, 15, 18, 24, 25, 27, 28, 30

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/576,439

DATE: 05/01/2006

TIME: 09:45:11

Input Set : A:\Seq.ST25.txt

Output Set: N:\CRF4\05012006\J576439.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16